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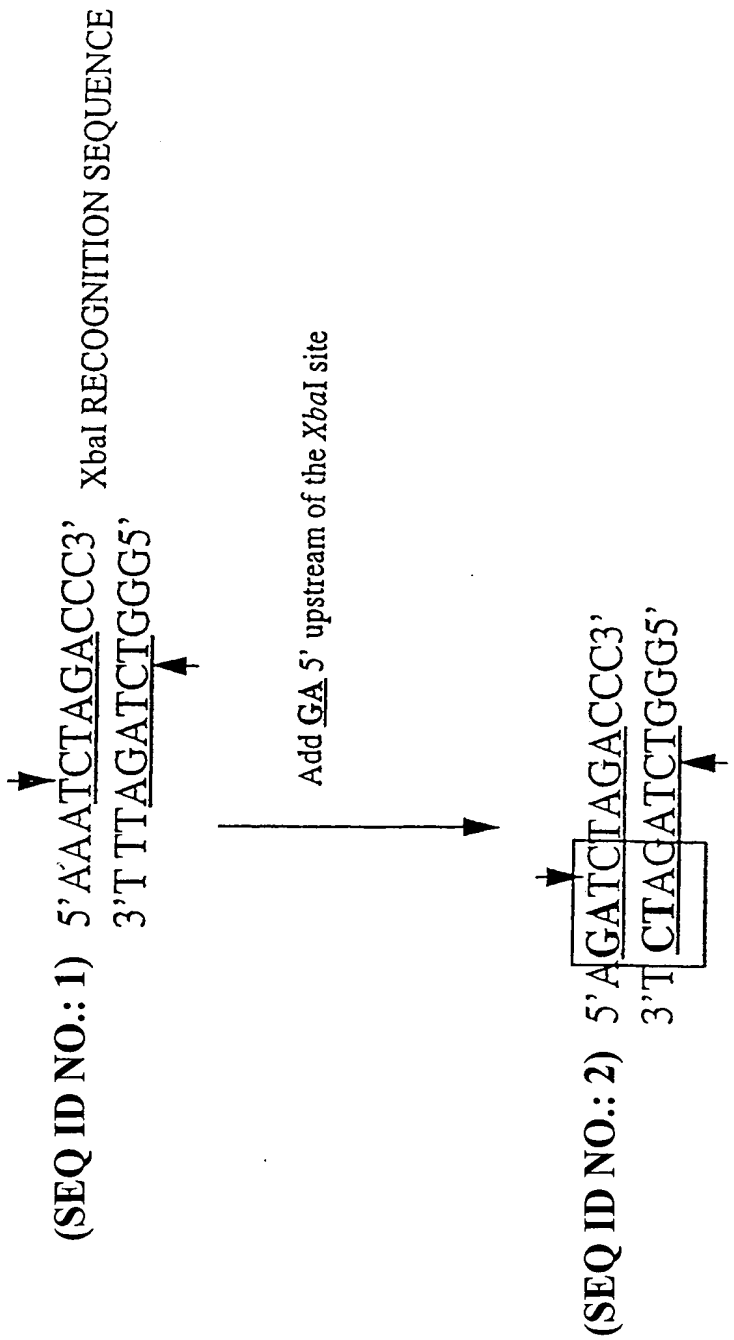

FIG.6.

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```
S.l.   1 MAGTDREKALDAALAQIERQFGKGAVMRMGDRTNEPIEVIPTGSTALDVA 50
         |||||||||||||||||||||||||||||||. ||||||||||||||||
S.a.   1 MAGTDREKALDAALAQIERQFGKGAVMRMGDRSKEPIEVIPTGSTALDVA 50
                .         .         .         .         .
      51 LGVGGIPRGRVVEVYGPESSGKTTLTLHAVANAQKAGGQVAFVDAEHALD 100
         |||||:|||||:|||||||||||||||||||||||||||||||||||||||
      51 LGVGGLPRGRVIEVYGPESSGKTTLTLHAVANAQKAGGQVAFVDAEHALD 100
                .         .         .         .         .
     101 PEYAKKLGVDIDNLILSQPDNGEQALEIVDMLVRSGALDLIVIDSVAALV 150
         ||||.|||||||||||||||||||||||||||||||||||||||||||||
     101 PEYAQKLGVDIDNLILSQPDNGEQALEIVDMLVRSGALDLIVIDSVAALV 150
                .         .         .         .         .
     151 PRAEIEGEMGDSHVGLQARLMSQALRKITSALNQSKTTAIFINQLREKIG 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 PRAEIEGEMGDSHVGLQARLMSQALRKITSALNQSKTTAIFINQLREKIG 200
                .         .         .         .         .
     201 VMFGSPETTTGGRALKFYASVRLDIRRIETLKDGTDAVGNRTRVKVVKNK 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 VMFGSPETTTGGRALKFYASVRLDIRRIETLKDGTDAVGNRTRVKVVKNK 250
                .         .         .         .         .
     251 VAPPFKQAEFDILYGQGISREGGLIDMGVENGFVRKAGAWYTYEGDQLGQ 300
         |||||||||||||||||||||||||||||.||||||||||||||||||||
     251 VAPPFKQAEFDILYGQGISREGGLIDMGVEHGFVRKAGAWYTYEGDQLGQ 300
                .         .         .         .         .
     301 GKENARNFLKDNPDLANEIEKKIKQKLGVGVHPEE.SATEPGADAASAAP 349
         |||||||||||||||||||||||:|||||| ||| .||| | |||.
     301 GKENARNFLKDNPDLANEIEKKIKEKLGVGVRPEEPTATESGPDAAT... 347
                .         .
     350 ADAAPAVPAPTTAKATKSKAAAAKS 374 (SEQ ID NO.: 3)
         |:.|||||||| ||| ||.|||||||
     348 AESAPAVPAPATAKVTKAKAAAAKS 372 (SEQ ID NO.: 4)
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FIG.13.

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S.l.    1 ATGGCAGGAACCGACCGCGAGAAGGCCCTGGACGCCGCGCTCGCACAGAT 50
        1 ATGGCAGGAACCGACCGCGAGAAGGCTCTTGACGCCGCACTCGCACAGAT 50
S.a.

       51 TGAACGGCAATTCGGCAAGGGCGCGGTCATGCGCATGGGTGACCGGACCA 100
       51 TGAACGGCAGTTCGGCAAGGGCGCGGTCATGCGCATGGGCGACCGGTCGA 100

      101 ACGAGCCCATCGAGGTCATCCCGACCGGGTCTACCGCGCTCGACGTGGCC 150
      101 AGGAGCCCATCGAGGTCATCCCGACCGGGTCGACCGCGCTCGACGTGGCC 150

      151 CTCGGCGTCGGAGGCATCCCGCGTGGCCGTGTCGTGGAGGTCTACGGCCC 200
      151 CTCGGCGTCGGCGGCCTGCCGCGCGGCCGCGTCATCGAGGTCTACGGTCC 200

      201 CGAGTCCTCGGGCAAGACGACCCTGACCCTGCACGCGGTGGCGAACGCGC 250
      201 GGAGTCCTCCGGTAAGACGACCCTGACCCTGCACGCCGTGGCGAACGCGC 250

      251 AGAAGGCCGGCGGCCAGGTCGCGTTCGTGGACGCCGAGCACGCCCTCGAC 300
      251 AGAAGGCCGGCGGCCAGGTGGCGTTCGTGGACGCGGAGCACGCCCTCGAC 300

      301 CCCGAGTACGCGAAGAAGCTCGGTGTCGACATCGACAACCTGATCCTGTC 350
      301 CCCGAGTACGCCCAGAAGCTCGGCGTCGACATCGACAACCTGATCCTGTC 350

      351 CCAGCCGGACAACGGTGAGCAGGCCCTGGAGATCGTGGACATGCTGGTCC 400
      351 CCAGCCGGACAACGGTGAGCAGGCCCTGGAGATCGTGGACATGCTGGTCC 400

      401 GCTCCGGCGCCCTCGACCTCATCGTCATCGACTCCGTCGCCGCGCTCGTC 450
      401 GCTCCGGCGCCCTCGACCTCATCGTCATCGACTCCGTCGCCGCGCTCGTC 450

      451 CCGCGCGCGGAGATCGAGGGCGAGATGGGCGACAGCCACGTCGGTCTGCA 500
      451 CCGCGCGCGGAGATCGAGGGCGAGATGGGTGACAGCCACGTCGGTCTCCA 500

      501 GGCCCGGCTGATGAGCCAGGCCCTGCGGAAGATCACCAGCGCGCTCAACC 550(SEQ ID NO.: 5)
      501 GGCCCGGCTGATGAGCCAGGCGCTCCGGAAGATCACCAGCGCGCTCAACC 550(SEQ ID NO.: 6)
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FIG.14.A.

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S.1.
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551 AGTCCAAGACCACCGCGATCTTCATCAACCAGCTCCGCGAGAAGATCGGC 600
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
```
S.a.
```
551 AGTCCAAGACCACCGCGATCTTCATCAACCAGCTCCGCGAGAAGATCGGC 600
    .         .         .         .         .
601 GTGATGTTCGGCTCCCCGGAGACCACGACCGGTGGCCGGGCACTGAAGTT 650
    || ||||||||||||||||||||||||||||||||||||| || |||||
601 GTCATGTTCGGCTCCCCGGAGACCACGACCGGTGGCCGGGCGCTCAAGTT 650
    .         .         .         .         .
651 CTACGCCTCGGTGCGACTCGACATCCGGCGTATCGAGACGCTGAAGGACG 700
    |||||||||||||||||||||||||| || |||||||||| |||||||
651 CTACGCCTCGGTGCGACTCGACATCCGACGCATCGAGACGCTCAAGGACG 700
    .         .         .         .         .
701 GCACCGACGCGGTCGGCAACCGCACCCGCGTCAAGGTGGTCAAGAACAAG 750
    |||||||||||||||||||||||| |||||||||| ||||||||||||
701 GCACCGACGCGGTCGGCAACCGCACGCGCGTCAAGGTCGTCAAGAACAAG 750
    .         .         .         .         .
751 GTCGCGCCGCCCTTCAAGCAGGCCGAGTTCGACATCCTCTACGGCCAGGG 800
    ||||||||||||||||||||||||||||||||||||||||||||||||||
751 GTCGCGCCGCCCTTCAAGCAGGCCGAGTTCGACATCCTCTACGGCCAGGG 800
    .         .         .         .         .
801 CATCAGCCGCGAGGGCGGTCTGATCGACATGGGCGTGGAGAACGGCTTCG 850
    |||||||||||||||||| |||||||||||||||||||| |||||||||
801 CATCAGCCGCGAGGGCGGCCTGATCGACATGGGCGTGGAGCACGGCTTCG 850
    .         .         .         .         .
851 TCCGCAAGGCCGGCGCCTGGTACACGTACGAGGGCGACCAGCTCGGTCAG 900
    |||||||||||||||||||||||||||||||||||||||||||||||| |||
851 TCCGCAAGGCCGGCGCCTGGTACACGTACGAGGGCGACCAGCTCGGCCAG 900
    .         .         .         .         .
901 GGCAAGGAGAACGCGCGCAACTTCCTGAAGGACAACCCCGACCTGGCCAA 950
    |||||||||||||||||||||||||||||||||||||||||||||| |||||
901 GGCAAGGAGAACGCGCGCAACTTCCTGAAGGACAACCCCGACCTCGCCAA 950
    .         .         .         .         .
951 CGAGATCGAGAAGAAGATCAAGCAGAAGCTGGGCGTCGGCGTGCACCCCG 1000
    |||||||||||||||||||| ||||||||||||||| || |  ||||
951 CGAGATCGAGAAGAAGATCAAGGAGAAGCTGGGCGTCGGAGTCCGTCCCG 1000
    .         .         .         .         .
1001 AGGA...GTCGGCCACCGAGCCCGGCGCGGACGCCGCCTCCGCCGCCCCG 1047
     ||||   | ||||||||||| |||| ||||         |||||| ||
1001 AGGAGCCGACGGCCACCGAGTCCGGACCGGA.........CGCCGCGACG 1041
     .         .         .         .         .
1048 GCCGACGCCGCACCGGCGGTGCCCGCACCCACGACCGCCAAGGCCACCAA 1097
     |||||  |||||||||||||||||| ||| ||||||||||| ||||||
1042 GCCGAATCCGCACCGGCGGTGCCCGCGCCCGCGACCGCCAAGGTCACCAA 1091
     .         .
1098 GTCCAAGGCCGCGGCAGCCAAGAGCTGA 1125 (SEQ ID NO.: 5)
     | ||||||||||||||||||||||||||
1092 GGCCAAGGCCGCGGCAGCCAAGAGCTGA 1119 (SEQ ID NO.: 6)
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FIG.14.B.